BACKCROSS BREEDING with RAPD MOLECULAR MARKERS to ENHANCE RESISTANCE to COMMON BACTERIAL BLIGHT in PINTO BEANS

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Common bacterial blight (CBB) in common bean (*Phaseolus vulgaris* L.), caused by *Xanthomonas campestris* pv. *phaseoli* (*Xcp*) reduces bean yields and quality throughout the world. Pinto 'Chase' (Coyne et al., 1994) is a high yielding rust resistant variety with moderate resistance to *Xcp* derived from great northern Nebraska #1 selection 27, whose resistance is derived from an unknown tepary (P. acutifolius) bean source. XAN-159 is a black mottled small seeded breeding line with genes for high resistance to *Xcp* that are different from those in GN Nebraska #1 sel 27 and are derived from a different tepary source (PI 319443). To provide for increased levels of resistance and for stability of resistance, efforts need to be made to recombine different resistance genes in the same genetic background or the different genes be introduced each into independent lines and utilized as genetic blends. Our objective was to pyramid different genes for *Xcp* resistance from the donor parent XAN-159 into the recurrent parent Pinto 'Chase' using the classical backcross breeding method and to confirm the incorporation of different genes using RAPD molecular markers.

Materials and Methods:

Backcross procedure: The cross Pinto 'Chase' x XAN-159 was made, and subsequently F1, BC1, BC2, and BC3 populations were generated using Pinto Chase as the recurrent parent. Selfed generations of BC1F2 and BC2F2 along with parents were grown using a randomized complete block design with three replications to confirm the resistance in segregating populations. Each block consisted of the BCF2 lines, two parents, and a susceptible check ('PC 50'). The experiments were conducted in the greenhouse, Lincoln, NE.

Inoculation: Two *Xcp* strains, one strain from Nebraska (EK-11) and one from Dominican Republic (DR-7) (source: A.K. Vidaver, Dept. of Plant Pathology, UNL) were used at 10^7 cfu with the multiple needle method (Andrus, 1948) to inoculate the first fully-developed leaves.

RAPD analysis: Total genomic DNA was extracted from lyophilized leaf tissue. Seven previously developed RAPD markers (Jung et.al., 1997) and one morphological marker (flower color, *V* locus) were confirmed in the BC1 and BC2 populations.

Result and Discussion

SFANOVA analysis showed that RAPD markers were significantly associated with resistance to *Xcp* in the backcross populations. Although the population used in this study was different from the mapping population 'PC 50 x XAN 159', the results indicated the value of these RAPD markers in breeding for resistance to *Xcp*.

Resistance was confirmed in some BC2F2 generation plants. Seven RAPD markers and the *V* locus (flower color) previously identified were confirmed in the BC1 and BC2 populations. Smaller seed size, purple flower color, and black mottled seed coat

color were coinherited with resistance to *Xcp*. However, a recombinant plant with enhanced CBB resistance and moderate sized pinto seed was identified. Backcross breeding is being continued.

Once all the favorable genes for resistance to *Xcp* are recovered in the genetic background of Pinto 'Chase' in advanced backcross generations (BC3Fn or BC4Fn), this germplasm would be expected to have improved resistance for common blight over the donor parent XAN 159, because Pinto 'Chase' also contributes a few recessive resistant genes. Thus, this germplasm can be used to introduce *Xcp* resistance to other susceptible or moderately susceptible but agronomically superior lines or to complement resistance in germplasm possessing different resistance genes. This germplasm would be expected to expedite common blight breeding programs because a few backcrosses would be enough to recover the genotype of the recurrent parents in pinto and great northern dry edible bean types. XAN-159 is considered exotic germplasm and differs in many agronomic and seed traits from GN and Pinto bean.

Literature Cited

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